Virulence in Puccina triticina and leaf rust resistance in hard red winter wheat.

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Leaf rust, caused by *Puccinia triticina*, is a common disease of hard red winter wheat in the Great Plains region of the U.S. In 2008, 52 races of leaf rust were described in the U.S. Races TDBGH (virulence to *Lr24*), MLDSD (virulence to *Lr39*/*Lr41*, and *Lr17*), TDBJH (virulence to *Lr24*) were among the most common races in the Great Plains region. Two major groups of *P. triticina,* based on simple sequence repeat (SSR) genotypes, are present in the Great Plains region. Isolates avirulent to *LrB*, *Lr17*, and *Lr3bg* are in one SSR group and are long established in North America. Isolates with virulence to *LrB*, *Lr17*, and *Lr3bg* are in a different SSR group and were likely introduced to the Great Plains region in the mid 1990s and increased with the widespread cultivation of Jagger with *Lr17*. Races with virulence to *Lr24*, *Lr26*, and *Lr39*/*Lr41* are found in both groups of SSR genotypes. Leaf rust resistance genes *Lr24*, *Lr17*, *Lr14a*, and *Lr39*/*Lr41* are very common in the hard red winter wheat cultivars. Genes *Lr16* and *Lr26* are present in fewer cultivars. Leaf rust races with virulence to these genes have been found in the hard red winter wheat area, thus none of these genes condition resistance to all leaf rust races. The adult-plant gene *Lr34* also is present in hard red winter wheat, however many cultivars derived from Jagger have an inactive allele at this locus. Preliminary results of genetic analysis of leaf rust resistance in the cultivar Duster indicated the presence of *Lr11*, an additional seedling-resistance gene, plus a functional allele of *Lr34* and an additional adult-plant resistance gene. The cultivar Santa Fe likely has the seedling resistance genes *Lr3* and *Lr17*, plus at least one adult-plant resistance gene that is likely not *Lr34*.

POSTER SESSION ABSTRACTS

Poster 1. Identification of quantitative trait loci associated with maintenance of bread-making quality under heat stress in wheat (Triticum aestivum).

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High temperature during reproductive development is a major factor limiting wheat production and end-use quality in the Southern Great Plains as well as in many other environments worldwide. We have initiated multiple projects integrating both genotypic and phenotypic data to identify quantitative trait loci (QTL) controlling reproductive stage heat tolerance in wheat, defined here as the maintenance of yield and end-use quality during reproductive-stage heat stress. In this study, we have focused on the mapping of QTL associated with end-use quality due to their importance and known sensitivity to heat stress. QTL mapping was carried out based on morphological, yield, and quality data from recombinant inbred lines (RILs) grown in controlled environments. The RILs were derived from the cross between Halberd, a heat-tolerant Australian line, and Cutter, an advanced line selected for its high score in yield and other agronomically important traits. RILs were phenotyped using the sodium dodecyl sulfate sedimentation (SDSS) test of grain harvested from heat-treatment greenhouse trials. Four QTL were identified: two associated with variation in SDSS levels under control conditions, one associated with variation in SDSS levels under heat stress conditions, and one associated with the maintenance of SDSS score between heat stress and control conditions. Identified QTL were confirmed in a population of advanced lines grown in field trials at three Texas nurseries. In addition, data from the advanced line trials was used to further analyze the identified QTL for their relation to yield and quality characteristics. An improved understanding of the correlation between end-use quality maintenance and yield stability QTL during reproductive stage heat stress will aid both in the breeding of plants possessing each attribute using marker-assisted selection and in basic research aimed at defining the molecular basis of heat tolerance.